

Sequence Listing PCT-JP03-00117.txt  
SEQUENCE LISTING

&lt;110&gt; Tetsuro Kokubo, Masahiro Shirakawa, and Jeremy Robin Howard Tame

&lt;120&gt; Method of monitoring gene expression

&lt;130&gt; 4439-4023

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; JP P2002-002396

&lt;151&gt; 2002-01-09

&lt;160&gt; 14

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2487

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2484)

&lt;400&gt; 1

atg ctg ttt gga gtg aag ttg gct aat gag gtt tat cct cct tgg aag	48
Met Leu Phe Gly Val Lys Leu Ala Asn Glu Val Tyr Pro Pro Trp Lys	
1 5 10 15	
ggt tct tat att aat tat gag ggc ttg aaa aaa ttc ctg aag gaa gat	96
Gly Ser Tyr Ile Asn Tyr Glu Gly Leu Lys Lys Phe Leu Lys Glu Asp	
20 25 30	
agc gtg aag gat gga agt aac gat aag aaa gca cgc tgg gac gat tca	144
Ser Val Lys Asp Gly Ser Asn Asp Lys Lys Ala Arg Trp Asp Asp Ser	
35 40 45	
gat gaa tcc aag ttt gtg gaa gag ttg gat aag gaa ctt gaa aaa gtc	192
Asp Glu Ser Lys Phe Val Glu Glu Leu Asp Lys Glu Leu Glu Lys Val	
50 55 60	
tat ggt ttt caa cta aaa aag tac aat aac ttg atg gag aga ttg tcc	240
Tyr Gly Phe Gln Leu Lys Lys Tyr Asn Asn Leu Met Glu Arg Leu Ser	
65 70 75 80	
cat ctg gag aaa caa aca gat acg gaa gca gcc ata aag gcc ttg gac	288
His Leu Glu Lys Gln Thr Asp Thr Glu Ala Ala Ile Lys Ala Leu Asp	
85 90 95	
gct gat gca ttc caa cgt gta ttg gag gaa ctg tta agc gag tct acc	336
Ala Asp Ala Phe Gln Arg Val Leu Glu Glu Leu Leu Ser Glu Ser Thr	
100 105 110	
gaa tta gac aat ttt aag aga ttg aac ttt act ggg ttt gct aag att	384
Glu Leu Asp Asn Phe Lys Arg Leu Asn Phe Thr Gly Phe Ala Lys Ile	
115 120 125	
gtt aag aaa cat gac aag cta tat cca aag tat cca tct gtt aaa tct	432
Val Lys Lys His Asp Lys Leu Tyr Pro Lys Tyr Pro Ser Val Lys Ser	
130 135 140	

## Sequence Listing PCT-JP03-00117.txt

ttg ttg gaa gtt aga tta aag gaa ttg cct tcc cat tcg gaa gaa tat	480
Leu Leu Glu Val Arg Leu Lys Glu Leu Pro Ser His Ser Glu Glu Tyr	145 150 155 160
tcc cca ttg ttg tat cgt att tca ttt ttg tac aac att ttg aga agt	528
Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser	165 170 175
aat ttt aac act gca tct gaa ccc tta gcc agc gct tct aag ttt tct	576
Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser	180 185 190
agc att gtc agc aat gac ata gac atg aat ttc aga agc ttt aaa ttt	624
Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe	195 200 205
tgg gtt cat aat gac aac tta atg gag gtc aaa aca aga atc ttg aga	672
Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg	210 215 220
cat ctt ccc gtg ttg gtc tac gcc aat gtt ccc tcc gaa aac gat gac	720
His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp	225 230 235 240
ctg gtc aat aga ttc gaa tca gat ata tca aat aat gat gaa att gtg	768
Leu Val Asn Arg Phe Glu Ser Asp Ile Ser Asn Asn Asp Glu Ile Val	245 250 255
ggt agt tcg agc tcc act agt agc gta gaa cat ggc ttg gga gcg cgc	816
Gly Ser Ser Ser Ser Thr Ser Ser Val Glu His Gly Leu Gly Ala Arg	260 265 270
tcc ttc gat cca tta atc aac acg cta tat ttt gac aat gag cat ttt	864
Ser Phe Asp Pro Leu Ile Asn Thr Leu Tyr Phe Asp Asn Glu His Phe	275 280 285
gaa tta tat aac gac aag tta tta aag tta aat tca gca cct act tta	912
Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu	290 295 300
aga tta agg tgg act ggc cag tta tct gat aag ccg gat att ttc ttg	960
Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu	305 310 315 320
gaa aag aaa act ctt att gaa gac gaa gcc act ggg aag tct gaa ttt	1008
Glu Lys Lys Thr Leu Ile Glu Asp Glu Ala Thr Gly Lys Ser Glu Phe	325 330 335
gat cta act aaa ttg caa ttg aaa caa aaa ttc att aac ggg ttt att	1056
Asp Leu Thr Lys Leu Gln Leu Lys Gln Lys Phe Ile Asn Gly Phe Ile	340 345 350
ttc gaa ggt gat aag aaa ttt aaa gaa caa act ttg aaa aag tta aaa	1104
Phe Glu Gly Asp Lys Lys Phe Lys Glu Gln Thr Leu Lys Lys Leu Lys	355 360 365
gaa agt ggt acg gca ggg aga gac ctg gaa agg tta gaa gaa gat ttc	1152
Glu Ser Gly Thr Ala Gly Arg Asp Leu Glu Arg Leu Glu Glu Asp Phe	370 375 380
tct gag att caa aac ttt att atc aag aat gaa ttg caa cca gtt ttt	1200
Ser Glu Ile Gln Asn Phe Ile Ile Lys Asn Glu Leu Gln Pro Val Phe	

## Sequence Listing PCT-JP03-00117.txt

385		390		395		400	
aga act gtt tac acc	aga act gct ttc cag att ccc ggc gat gac aag						1248
Arg Thr Val Tyr Thr	Arg Thr Ala Phe Gln Ile Pro Gly Asp Asp Lys						
		405		410		415	
ata aga gta acc att	gac tct aat att gta ttc atc aag gag gat tca						1296
Ile Arg Val Thr Ile	Asp Ser Asn Ile Val Phe Ile Lys Glu Asp Ser						
		420		425		430	
ttc gac aga gag cgt	cca att aga gac cct aat acc tgg cat aga act						1344
Phe Asp Arg Glu Arg	Pro Ile Arg Asp Pro Asn Thr Trp His Arg Thr						
		435		440		445	
gat att gat gcc aat	gtt gca aat ccc ttg aaa ttc ctg aga gga ggc						1392
Asp Ile Asp Ala Asn	Val Ala Asn Pro Leu Lys Phe Leu Arg Gly Gly						
		450		455		460	
gag tat gct aag ttt	cct tat tca gta atg gaa att aaa gtg aaa agt						1440
Glu Tyr Ala Lys Phe	Pro Tyr Ser Val Met Glu Ile Lys Val Lys Ser						
		470		475		480	
tca tta gat tct tcg	atg tct gcc agt tct atg att tct aat gta aaa						1488
Ser Leu Asp Ser Ser	Met Ser Ala Ser Ser Met Ile Ser Asn Val Lys						
		485		490		495	
ctg cct aaa aag cat	ggt caa tgg ctg aac gat ttg aca aat tct cat						1536
Leu Pro Lys Lys His	Gly Gln Trp Leu Asn Asp Leu Thr Asn Ser His						
		500		505		510	
ttg gtc aaa gaa att	cca aag ttt tct atc ttt gtg caa ggt gtg gca						1584
Leu Val Lys Glu Ile	Pro Lys Phe Ser Ile Phe Val Gln Gly Val Ala						
		515		520		525	
tca ttg tat gga gat	gat gaa aaa tta gat atc tta cca ttt tgg tta						1632
Ser Leu Tyr Gly Asp	Asp Glu Lys Leu Asp Ile Leu Pro Phe Trp Leu						
		530		535		540	
cca gat ttg gaa aca	gat att aga cag gat cct aag caa gca tat gag						1680
Pro Asp Leu Glu Thr	Asp Ile Arg Gln Asp Pro Lys Gln Ala Tyr Glu						
		545		550		555	
gag gaa aag aaa aaa	ctg ttg aaa caa aaa gag ata caa aag aaa att						1728
Glu Glu Lys Lys Lys	Leu Leu Lys Gln Lys Glu Ile Gln Lys Lys Ile						
		565		570		575	
gat gga atg aga agg	ctt tcc aac tta aaa gag cct caa cat caa gca						1776
Asp Gly Met Arg Arg	Leu Ser Asn Leu Lys Glu Pro Gln His Gln Ala						
		580		585		590	
gca gta ccg gta tct	caa gag gaa aat gag cgt att acc tct caa ggt						1824
Ala Val Pro Val Ser	Gln Glu Glu Asn Glu Arg Ile Thr Ser Gln Gly						
		595		600		605	
gat ttg gag gca gac	ggt tca tcc gat gag gaa act gag caa gaa cct						1872
Asp Leu Glu Ala Asp	Gly Ser Ser Asp Glu Glu Thr Glu Gln Glu Pro						
		610		615		620	
cat tcg aaa aga tca	aag aaa gtt cgg aga aga aaa ccc aag gcc act						1920
His Ser Lys Arg Ser	Lys Lys Val Arg Arg Arg Lys Pro Lys Ala Thr						
		625		630		635	
ttc ttg aga att ttg	gcc ggt aga gat cca aag tta atg ggg gtg gat						1968

Sequence Listing PCT-JP03-00117.txt

Phe	Leu	Arg	Ile	Leu	Ala	Gly	Arg	Asp	Pro	Lys	Leu	Met	Gly	Val	Asp	
				645					650					655		
tct	gaa	gaa	gaa	gaa	att	gaa	ttg	cca	cct	ggt	gtg	aaa	aaa	cca	tta	2016
Ser	Glu	Glu	Glu	Glu	Ile	Glu	Leu	Pro	Pro	Gly	Val	Lys	Lys	Pro	Leu	
			660					665					670			
aat	ttg	tta	aaa	aat	gct	ggt	cct	gta	aac	gtg	gag	gca	aag	gtt	tgg	2064
Asn	Leu	Leu	Lys	Asn	Ala	Gly	Pro	Val	Asn	Val	Glu	Ala	Lys	Val	Trp	
		675					680					685				
ctt	gcc	aac	gaa	cgt	aca	ttt	aac	aga	tgg	tta	agt	gtc	acc	agt	tta	2112
Leu	Ala	Asn	Glu	Arg	Thr	Phe	Asn	Arg	Trp	Leu	Ser	Val	Thr	Ser	Leu	
	690					695					700					
ttg	agt	gtt	ttg	acg	ttc	tca	att	tat	aat	tct	gtg	aag	aaa	gcc	gaa	2160
Leu	Ser	Val	Leu	Thr	Phe	Ser	Ile	Tyr	Asn	Ser	Val	Lys	Lys	Ala	Glu	
	705				710					715					720	
tac	ccc	act	ttg	gct	aac	tac	atg	gca	tac	gta	tat	ttt	ggt	cta	acg	2208
Tyr	Pro	Thr	Leu	Ala	Asn	Tyr	Met	Ala	Tyr	Val	Tyr	Phe	Gly	Leu	Thr	
				725					730					735		
ata	ttc	tgt	gct	tta	tgg	tcc	tat	tcc	att	tat	atg	aaa	aga	gtt	gat	2256
Ile	Phe	Cys	Ala	Leu	Trp	Ser	Tyr	Ser	Ile	Tyr	Met	Lys	Arg	Val	Asp	
			740					745					750			
att	att	caa	caa	aga	agc	ggt	caa	cat	cta	gat	gca	cca	ctt	ggt	cca	2304
Ile	Ile	Gln	Gln	Arg	Ser	Gly	Gln	His	Leu	Asp	Ala	Pro	Leu	Gly	Pro	
		755				760						765				
gtt	ttg	gtt	tct	ata	gtt	tta	ttt	gtc	act	tta	gtg	gtt	aat	ttt	gtt	2352
Val	Leu	Val	Ser	Ile	Val	Leu	Phe	Val	Thr	Leu	Val	Val	Asn	Phe	Val	
	770					775					780					
atg	gcg	ttt	aga	aat	gca	gca	aag	tct	cgt	caa	gag	ttg	caa	ata	cag	2400
Met	Ala	Phe	Arg	Asn	Ala	Ala	Lys	Ser	Arg	Gln	Glu	Leu	Gln	Ile	Gln	
					790					795					800	
aat	tta	gaa	gtt	cct	gaa	aga	ata	cca	gaa	gta	tta	agg	cca	ctt	caa	2448
Asn	Leu	Glu	Val	Pro	Glu	Arg	Ile	Pro	Glu	Val	Leu	Arg	Pro	Leu	Gln	
				805					810					815		
aat	tat	cta	ttc	aag	tta	atg	ggg	cca	agc	agt	gat	tag				2487
Asn	Tyr	Leu	Phe	Lys	Leu	Met	Gly	Pro	Ser	Ser	Asp					
			820					825								

<210> 2

<211> 828

<212> PRT

<213> Saccharomyces cerevisiae

<400> 2

Met Leu Phe Gly Val Lys Leu Ala Asn Glu Val Tyr Pro Pro Trp Lys  
1 5 10 15

Gly Ser Tyr Ile Asn Tyr Glu Gly Leu Lys Lys Phe Leu Lys Glu Asp  
20 25 30

Ser Val Lys Asp Gly Ser Asn Asp Lys Lys Ala Arg Trp Asp Asp Ser  
35 40 45

Sequence Listing PCT-JP03-00117.txt

Asp Glu Ser Lys Phe Val Glu Glu Leu Asp Lys Glu Leu Glu Lys Val  
 50 55 60  
 Tyr Gly Phe Gln Leu Lys Lys Tyr Asn Asn Leu Met Glu Arg Leu Ser  
 65 70 75 80  
 His Leu Glu Lys Gln Thr Asp Thr Glu Ala Ala Ile Lys Ala Leu Asp  
 85 90 95  
 Ala Asp Ala Phe Gln Arg Val Leu Glu Glu Leu Leu Ser Glu Ser Thr  
 100 105 110  
 Glu Leu Asp Asn Phe Lys Arg Leu Asn Phe Thr Gly Phe Ala Lys Ile  
 115 120 125  
 Val Lys Lys His Asp Lys Leu Tyr Pro Lys Tyr Pro Ser Val Lys Ser  
 130 135 140  
 Leu Leu Glu Val Arg Leu Lys Glu Leu Pro Ser His Ser Glu Glu Tyr  
 145 150 155 160  
 Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser  
 165 170 175  
 Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser  
 180 185 190  
 Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe  
 195 200 205  
 Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg  
 210 215 220  
 His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp  
 225 230 235 240  
 Leu Val Asn Arg Phe Glu Ser Asp Ile Ser Asn Asn Asp Glu Ile Val  
 245 250 255  
 Gly Ser Ser Ser Ser Thr Ser Ser Val Glu His Gly Leu Gly Ala Arg  
 260 265 270  
 Ser Phe Asp Pro Leu Ile Asn Thr Leu Tyr Phe Asp Asn Glu His Phe  
 275 280 285  
 Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu  
 290 295 300  
 Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu  
 305 310 315 320  
 Glu Lys Lys Thr Leu Ile Glu Asp Glu Ala Thr Gly Lys Ser Glu Phe  
 325 330 335  
 Asp Leu Thr Lys Leu Gln Leu Lys Gln Lys Phe Ile Asn Gly Phe Ile  
 340 345 350  
 Phe Glu Gly Asp Lys Lys Phe Lys Glu Gln Thr Leu Lys Lys Leu Lys  
 355 360 365  
 Glu Ser Gly Thr Ala Gly Arg Asp Leu Glu Arg Leu Glu Glu Asp Phe  
 370 375 380

Sequence Listing PCT-JP03-00117.txt

Ser Glu Ile Gln Asn Phe Ile Ile Lys Asn Glu Leu Gln Pro Val Phe  
385 390 395 400

Arg Thr Val Tyr Thr Arg Thr Ala Phe Gln Ile Pro Gly Asp Asp Lys  
405 410 415

Ile Arg Val Thr Ile Asp Ser Asn Ile Val Phe Ile Lys Glu Asp Ser  
420 425 430

Phe Asp Arg Glu Arg Pro Ile Arg Asp Pro Asn Thr Trp His Arg Thr  
435 440 445

Asp Ile Asp Ala Asn Val Ala Asn Pro Leu Lys Phe Leu Arg Gly Gly  
450 455 460

Glu Tyr Ala Lys Phe Pro Tyr Ser Val Met Glu Ile Lys Val Lys Ser  
465 470 475 480

Ser Leu Asp Ser Ser Met Ser Ala Ser Ser Met Ile Ser Asn Val Lys  
485 490 495

Leu Pro Lys Lys His Gly Gln Trp Leu Asn Asp Leu Thr Asn Ser His  
500 505 510

Leu Val Lys Glu Ile Pro Lys Phe Ser Ile Phe Val Gln Gly Val Ala  
515 520 525

Ser Leu Tyr Gly Asp Asp Glu Lys Leu Asp Ile Leu Pro Phe Trp Leu  
530 535 540

Pro Asp Leu Glu Thr Asp Ile Arg Gln Asp Pro Lys Gln Ala Tyr Glu  
545 550 555 560

Glu Glu Lys Lys Lys Leu Leu Lys Gln Lys Glu Ile Gln Lys Lys Ile  
565 570 575

Asp Gly Met Arg Arg Leu Ser Asn Leu Lys Glu Pro Gln His Gln Ala  
580 585 590

Ala Val Pro Val Ser Gln Glu Glu Asn Glu Arg Ile Thr Ser Gln Gly  
595 600 605

Asp Leu Glu Ala Asp Gly Ser Ser Asp Glu Glu Thr Glu Gln Glu Pro  
610 615 620

His Ser Lys Arg Ser Lys Lys Val Arg Arg Arg Lys Pro Lys Ala Thr  
625 630 635 640

Phe Leu Arg Ile Leu Ala Gly Arg Asp Pro Lys Leu Met Gly Val Asp  
645 650 655

Ser Glu Glu Glu Glu Ile Glu Leu Pro Pro Gly Val Lys Lys Pro Leu  
660 665 670

Asn Leu Leu Lys Asn Ala Gly Pro Val Asn Val Glu Ala Lys Val Trp  
675 680 685

Leu Ala Asn Glu Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Ser Leu  
690 695 700

Leu Ser Val Leu Thr Phe Ser Ile Tyr Asn Ser Val Lys Lys Ala Glu  
705 710 715 720

Sequence Listing (Continued)															
Tyr	Pro	Thr	Leu	Ala	Asn	Tyr	Met	Ala	Tyr	Val	Tyr	Phe	Gly	Leu	Thr
				725					730					735	
Ile	Phe	Cys	Ala	Leu	Trp	Ser	Tyr	Ser	Ile	Tyr	Met	Lys	Arg	Val	Asp
				740					745					750	
Ile	Ile	Gln	Gln	Arg	Ser	Gly	Gln	His	Leu	Asp	Ala	Pro	Leu	Gly	Pro
				755					760					765	
Val	Leu	Val	Ser	Ile	Val	Leu	Phe	Val	Thr	Leu	Val	Val	Asn	Phe	Val
				770					775					780	
Met	Ala	Phe	Arg	Asn	Ala	Ala	Lys	Ser	Arg	Gln	Glu	Leu	Gln	Ile	Gln
				785					790					795	800
Asn	Leu	Glu	Val	Pro	Glu	Arg	Ile	Pro	Glu	Val	Leu	Arg	Pro	Leu	Gln
				805					810					815	
Asn	Tyr	Leu	Phe	Lys	Leu	Met	Gly	Pro	Ser	Ser	Asp				
				820					825						

```
<210> 3
<211> 2508
<212> DNA
<213> Saccharomyces cerevisiae
```

```
<220>  
<221> CDS  
<222> (1)..(2505)
```

[illegible]

## Sequence Listing PCT-JP03-00117.txt

115	120	125	
aag Lys	aaa Lys 130	cac His	gat Asp 135
aaa Lys	tta Leu	cat His 135	cca Pro
aac Asn	tat Tyr	cct Pro	tct Ser 140
gta Val	aag Lys	tct Ser	ctt Leu
432			
tta Leu 145	caa Gln	gtc Val	aga Arg
ttg Leu	aaa Lys 150	gaa Glu	ctt Leu
cct Pro	ttc Phe	aac Asn 155	aat Asn
tca Ser	gaa Glu	gag Glu	tat Tyr 160
480			
tct Ser	ccc Pro	ttg Leu	ttg Leu
tat Tyr 165	agg Arg	atc Ile	tca Ser
ctg Leu 170	tac Tyr	gag Glu	ttc Phe
528			
aat Asn	tat Tyr	gat Asp 180	cat His 180
cca Pro	aat Asn	acg Thr	gtg Val 185
tct Ser 185	aaa Lys	tca Ser	tta Leu
gca Ala	agt Ser 190	act Thr	tct Ser
576			
aaa Lys	tta Leu	tca Ser 195	cat His
ttt Phe	tct Ser	aac Asn	ctt Leu 200
gaa Glu	gac Asp	gca Ala	agt Ser 205
624			
aag Lys	ttt Phe 210	tgg Trp	gtt Val
cat His	gat Asp	gat Asp 215	aat Asn
ata Ile	atg Met	gag Glu	gtt Val 220
672			
tta Leu 225	agg Arg	cat His	cta Leu
cct Pro	gct Ala 230	ttg Leu	gtt Val
tat Tyr	gcg Ala	tcg Ser 235	gtt Val
720			
gac Asp	gat Asp	ttc Phe	gtc Val 245
aat Asn	cta Leu	gaa Glu	tca Ser
gat Asp 250	gtc Val	cgc Arg	gta Val
768			
gag Ala	cgc Arg	ttg Leu	aat Asn 260
att Ile	ggt Gly	tca Ser	aag Lys
agt Ser 265	aac Asn	agc Ser	ctt Leu
816			
aat Asn	agc Ser 275	aac Gln	gat Asp
gtt Val	gaa Glu	att Ile 280	gga Gly
aaa Lys	tca Ser	aag Lys	agc Ser 285
864			
cca Pro	cag Gln 290	tca Ser	tat Tyr
gat Asp	cca Pro	aca Thr 295	atc Ile
act Thr	aca Thr	tta Leu	tat Tyr 300
912			
ttt Phe 305	ttt Phe	gat Asp	ttg Leu
tac Tyr	aat Asn 310	aac Asn	aga Arg
ttg Leu	aaa Lys 315	atc Ile	agc Ser
960			
acg Thr	ctg Leu	aga Leu	gac Asp
aaa Lys	ctg Leu	aaa Lys	cct Pro
gac Asp 330	aaa Lys	cct Pro	gac Asp 335
1008			
ttt Phe	ttg Leu	gaa Glu	aag Lys
aga Arg	act Thr	ttt Phe	aca Thr
gaa Glu 340	aaa Lys 345	acc Thr	gaa Glu
1056			
agt Ser	ttt Phe	gaa Glu 355	gaa Glu
atc Ile	aga Arg	ttg Leu	caa Gln 360
atg Met	aaa Lys	gcc Ala	aaa Lys
1104			
ttt Phe	att Tyr	aaa Lys	aat Asn
att Tyr	aaa Lys	aat Asn	caa Asn
1152			



## Sequence Listing PCT-JP03-00117.txt

Phe	Ile	Phe	Lys	Asn	Asp	Pro	Ser	Tyr	Lys	Asn	Tyr	Leu	Ile	Asn	Gln	
370						375					380					
cta	aga	gaa	agg	ggg	act	caa	aag	gag	gaa	ctg	gaa	aaa	ctt	tct	aga	1200
Leu	Arg	Glu	Arg	Gly	Thr	Gln	Lys	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Arg	
385					390					395					400	
gac	ttt	gat	aac	atc	caa	aac	ttt	att	ggt	gag	gag	aag	ttg	cag	cca	1248
Asp	Phe	Asp	Asn	Ile	Gln	Asn	Phe	Ile	Val	Glu	Glu	Lys	Leu	Gln	Pro	
				405					410					415		
ggt	ttg	aga	gct	acc	tat	aat	aga	act	gct	ttc	caa	att	cct	gga	gat	1296
Val	Leu	Arg	Ala	Thr	Tyr	Asn	Arg	Thr	Ala	Phe	Gln	Ile	Pro	Gly	Asp	
			420					425					430			
caa	agt	att	aga	gtc	act	atc	gat	tcc	aat	atc	atg	tac	att	aga	gag	1344
Gln	Ser	Ile	Arg	Val	Thr	Ile	Asp	Ser	Asn	Ile	Met	Tyr	Ile	Arg	Glu	
		435					440					445				
gat	tct	ttg	gac	aaa	aat	agg	ccc	att	agg	aac	cct	gag	aat	tgg	cac	1392
Asp	Ser	Leu	Asp	Lys	Asn	Arg	Pro	Ile	Arg	Asn	Pro	Glu	Asn	Trp	His	
	450					455					460					
cgt	gac	gat	att	gat	tcc	aat	att	ccc	aac	cca	ttg	agg	ttt	tta	aga	1440
Arg	Asp	Asp	Ile	Asp	Ser	Asn	Ile	Pro	Asn	Pro	Leu	Arg	Phe	Leu	Arg	
465					470					475					480	
gca	gga	gaa	tat	tcg	aag	ttc	ccc	tat	tct	gta	atg	gag	att	aag	gtt	1488
Ala	Gly	Glu	Tyr	Ser	Lys	Phe	Pro	Tyr	Ser	Val	Met	Glu	Ile	Lys	Val	
				485					490					495		
ata	aac	caa	gat	aat	tct	caa	atg	cct	aat	tat	gag	tgg	att	aaa	gat	1536
Ile	Asn	Gln	Asp	Asn	Ser	Gln	Met	Pro	Asn	Tyr	Glu	Trp	Ile	Lys	Asp	
			500					505					510			
tta	act	aat	tca	cat	tta	gtt	aac	gaa	gtt	cca	aaa	ttt	tct	ttg	tac	1584
Leu	Thr	Asn	Ser	His	Leu	Val	Asn	Glu	Val	Pro	Lys	Phe	Ser	Leu	Tyr	
		515					520					525				
ttg	caa	ggg	gtg	gct	tca	ctg	ttt	ggg	gaa	gac	gat	aaa	tat	gtc	aac	1632
Leu	Gln	Gly	Val	Ala	Ser	Leu	Phe	Gly	Glu	Asp	Asp	Lys	Tyr	Val	Asn	
	530					535					540					
att	ttg	cca	ttc	tgg	ttg	ccc	gat	tta	gaa	acc	gac	atc	aga	aag	aac	1680
Ile	Leu	Pro	Phe	Trp	Leu	Pro	Asp	Leu	Glu	Thr	Asp	Ile	Arg	Lys	Asn	
545					550					555					560	
cct	cag	gag	gct	tac	gaa	gaa	gag	aag	aaa	act	tta	caa	aaa	caa	aag	1728
Pro	Gln	Glu	Ala	Tyr	Glu	Glu	Glu	Lys	Lys	Thr	Leu	Gln	Lys	Gln	Lys	
				565					570					575		
agc	att	cat	gat	aaa	ctt	gat	aat	atg	aga	agg	tta	tcc	aaa	atc	tct	1776
Ser	Ile	His	Asp	Lys	Leu	Asp	Asn	Met	Arg	Arg	Leu	Ser	Lys	Ile	Ser	
			580					585					590			
gta	cca	gat	gga	aag	acc	act	gaa	aga	caa	ggg	caa	aaa	gat	cag	aat	1824
Val	Pro	Asp	Gly	Lys	Thr	Thr	Glu	Arg	Gln	Gly	Gln	Lys	Asp	Gln	Asn	
		595					600					605				
act	cgc	cac	gtt	att	gca	gat	tta	gaa	gat	cac	gaa	tca	tca	gat	gaa	1872
Thr	Arg	His	Val	Ile	Ala	Asp	Leu	Glu	Asp	His	Glu	Ser	Ser	Asp	Glu	
	610					615					620					

## Sequence Listing PCT-JP03-00117.txt

gaa ggt act gca ttg ccc aag aaa tct gca gtc aaa aaa ggg aag aaa Glu Gly Thr Ala Leu Pro Lys Lys Ser Ala Val Lys Lys Gly Lys Lys 625 630 635 640	1920
ttc aaa acg aat gca gct ttc ttg aaa att ctt gct gga aaa aat att Phe Lys Thr Asn Ala Ala Phe Leu Lys Ile Leu Ala Gly Lys Asn Ile 645 650 655	1968
tca gaa aat gga aat gat cca tac tcc gac gat aca gac agt gcc tct Ser Glu Asn Gly Asn Asp Pro Tyr Ser Asp Asp Thr Asp Ser Ala Ser 660 665 670	2016
tct ttc caa tta cct ccg gga gtt aaa aaa cca gtt cac ctt ttg aaa Ser Phe Gln Leu Pro Pro Gly Val Lys Lys Pro Val His Leu Leu Lys 675 680 685	2064
aat gcc ggt cct gtc aaa gtt gag gca aaa gtt tgg ctc gcc aat gaa Asn Ala Gly Pro Val Lys Val Glu Ala Lys Val Trp Leu Ala Asn Glu 690 695 700	2112
cgt aca ttc aat aga tgg tta agt gta acc aca ttg ctg agt gta ttg Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Thr Leu Leu Ser Val Leu 705 710 715 720	2160
acc ttt tct atc tat aat tca gtg caa aaa gcc gaa ttt cca caa cta Thr Phe Ser Ile Tyr Asn Ser Val Gln Lys Ala Glu Phe Pro Gln Leu 725 730 735	2208
gct gat ctg ttg gcc tat gta tat ttc ttt ttg act ttg ttt tgc gga Ala Asp Leu Leu Ala Tyr Val Tyr Phe Phe Leu Thr Leu Phe Cys Gly 740 745 750	2256
gta tgg gct tat aga acc tac tta aaa aga tta act ctt att aaa ggt Val Trp Ala Tyr Arg Thr Tyr Leu Lys Arg Leu Thr Leu Ile Lys Gly 755 760 765	2304
aga agt ggt aag cat ttg gat gca cct gtg gga cct att ttg gtt gca Arg Ser Gly Lys His Leu Asp Ala Pro Val Gly Pro Ile Leu Val Ala 770 775 780	2352
gtt gta tta atc gtt acc ttg gtt gtt aac ttt agt gtg gct ttt aaa Val Val Leu Ile Val Thr Leu Val Val Asn Phe Ser Val Ala Phe Lys 785 790 795 800	2400
gag gcc gct agg agg gaa aga gga tta gta aac gtt tcc tcc cag cct Glu Ala Ala Arg Arg Glu Arg Gly Leu Val Asn Val Ser Ser Gln Pro 805 810 815	2448
tcg tta ccc cgt aca cta aaa cca att caa gat ttt atc ttc aat ttg Ser Leu Pro Arg Thr Leu Lys Pro Ile Gln Asp Phe Ile Phe Asn Leu 820 825 830	2496
gtt ggg gaa taa Val Gly Glu 835	2508

<210> 4  
 <211> 835  
 <212> PRT  
 <213> Saccharomyces cerevisiae  
 <400> 4

## Sequence Listing PCT-JP03-00117.txt

Met Leu Phe Gly Ile Lys Leu Ala Asn Asp Val Tyr Pro Pro Trp Lys  
 1 5 10 15  
 Asp Ser Tyr Ile Asp Tyr Glu Arg Leu Lys Lys Leu Leu Lys Glu Ser  
 20 25 30  
 Val Ile His Asp Gly Arg Ser Ser Val Asp Ser Trp Ser Glu Arg Asn  
 35 40 45  
 Glu Ser Asp Phe Val Glu Ala Leu Asp Lys Glu Leu Glu Lys Val Tyr  
 50 55 60  
 Thr Phe Gln Ile Ser Lys Tyr Asn Ala Val Leu Arg Lys Leu Asp Asp  
 65 70 75 80  
 Leu Glu Glu Asn Thr Lys Ser Ala Glu Lys Ile Gln Lys Ile Asn Ser  
 85 90 95  
 Glu Gln Phe Lys Asn Thr Leu Glu Glu Cys Leu Asp Glu Ala Gln Arg  
 100 105 110  
 Leu Asp Asn Phe Asp Arg Leu Asn Phe Thr Gly Phe Ile Lys Ile Val  
 115 120 125  
 Lys Lys His Asp Lys Leu His Pro Asn Tyr Pro Ser Val Lys Ser Leu  
 130 135 140  
 Leu Gln Val Arg Leu Lys Glu Leu Pro Phe Asn Asn Ser Glu Glu Tyr  
 145 150 155 160  
 Ser Pro Leu Leu Tyr Arg Ile Ser Tyr Leu Tyr Glu Phe Leu Arg Ser  
 165 170 175  
 Asn Tyr Asp His Pro Asn Thr Val Ser Lys Ser Leu Ala Ser Thr Ser  
 180 185 190  
 Lys Leu Ser His Phe Ser Asn Leu Glu Asp Ala Ser Phe Lys Ser Tyr  
 195 200 205  
 Lys Phe Trp Val His Asp Asp Asn Ile Met Glu Val Lys Ala Arg Ile  
 210 215 220  
 Leu Arg His Leu Pro Ala Leu Val Tyr Ala Ser Val Pro Asn Glu Asn  
 225 230 235 240  
 Asp Asp Phe Val Asp Asn Leu Glu Ser Asp Val Arg Val Gln Pro Glu  
 245 250 255  
 Ala Arg Leu Asn Ile Gly Ser Lys Ser Asn Ser Leu Ser Ser Asp Gly  
 260 265 270  
 Asn Ser Asn Gln Asp Val Glu Ile Gly Lys Ser Lys Ser Val Ile Phe  
 275 280 285  
 Pro Gln Ser Tyr Asp Pro Thr Ile Thr Thr Leu Tyr Phe Asp Asn Asp  
 290 295 300  
 Phe Phe Asp Leu Tyr Asn Asn Arg Leu Leu Lys Ile Ser Gly Ala Pro  
 305 310 315 320  
 Thr Leu Arg Leu Arg Trp Ile Gly Lys Leu Leu Asp Lys Pro Asp Ile  
 325 330 335

## Sequence Listing PCT-JP03-00117.txt

Phe Leu Glu Lys Arg Thr Phe Thr Glu Asn Thr Glu Thr Gly Asn Ser  
 340 345 350  
 Ser Phe Glu Glu Ile Arg Leu Gln Met Lys Ala Lys Phe Ile Asn Asn  
 355 360 365  
 Phe Ile Phe Lys Asn Asp Pro Ser Tyr Lys Asn Tyr Leu Ile Asn Gln  
 370 375 380  
 Leu Arg Glu Arg Gly Thr Gln Lys Glu Glu Leu Glu Lys Leu Ser Arg  
 385 390 395 400  
 Asp Phe Asp Asn Ile Gln Asn Phe Ile Val Glu Glu Lys Leu Gln Pro  
 405 410 415  
 Val Leu Arg Ala Thr Tyr Asn Arg Thr Ala Phe Gln Ile Pro Gly Asp  
 420 425 430  
 Gln Ser Ile Arg Val Thr Ile Asp Ser Asn Ile Met Tyr Ile Arg Glu  
 435 440 445  
 Asp Ser Leu Asp Lys Asn Arg Pro Ile Arg Asn Pro Glu Asn Trp His  
 450 455 460  
 Arg Asp Asp Ile Asp Ser Asn Ile Pro Asn Pro Leu Arg Phe Leu Arg  
 465 470 475 480  
 Ala Gly Glu Tyr Ser Lys Phe Pro Tyr Ser Val Met Glu Ile Lys Val  
 485 490 495  
 Ile Asn Gln Asp Asn Ser Gln Met Pro Asn Tyr Glu Trp Ile Lys Asp  
 500 505 510  
 Leu Thr Asn Ser His Leu Val Asn Glu Val Pro Lys Phe Ser Leu Tyr  
 515 520 525  
 Leu Gln Gly Val Ala Ser Leu Phe Gly Glu Asp Asp Lys Tyr Val Asn  
 530 535 540  
 Ile Leu Pro Phe Trp Leu Pro Asp Leu Glu Thr Asp Ile Arg Lys Asn  
 545 550 555 560  
 Pro Gln Glu Ala Tyr Glu Glu Glu Lys Lys Thr Leu Gln Lys Gln Lys  
 565 570 575  
 Ser Ile His Asp Lys Leu Asp Asn Met Arg Arg Leu Ser Lys Ile Ser  
 580 585 590  
 Val Pro Asp Gly Lys Thr Thr Glu Arg Gln Gly Gln Lys Asp Gln Asn  
 595 600 605  
 Thr Arg His Val Ile Ala Asp Leu Glu Asp His Glu Ser Ser Asp Glu  
 610 615 620  
 Glu Gly Thr Ala Leu Pro Lys Lys Ser Ala Val Lys Lys Gly Lys Lys  
 625 630 635 640  
 Phe Lys Thr Asn Ala Ala Phe Leu Lys Ile Leu Ala Gly Lys Asn Ile  
 645 650 655  
 Ser Glu Asn Gly Asn Asp Pro Tyr Ser Asp Asp Thr Asp Ser Ala Ser  
 660 665 670

Sequence Listing PCT-JP03-00117.txt

Ser Phe Gln Leu Pro Pro Gly Val Lys Lys Pro Val His Leu Leu Lys  
675 680 685

Asn Ala Gly Pro Val Lys Val Glu Ala Lys Val Trp Leu Ala Asn Glu  
690 695 700

Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Thr Leu Leu Ser Val Leu  
705 710 715 720

Thr Phe Ser Ile Tyr Asn Ser Val Gln Lys Ala Glu Phe Pro Gln Leu  
725 730 735

Ala Asp Leu Leu Ala Tyr Val Tyr Phe Phe Leu Thr Leu Phe Cys Gly  
740 745 750

Val Trp Ala Tyr Arg Thr Tyr Leu Lys Arg Leu Thr Leu Ile Lys Gly  
755 760 765

Arg Ser Gly Lys His Leu Asp Ala Pro Val Gly Pro Ile Leu Val Ala  
770 775 780

Val Val Leu Ile Val Thr Leu Val Val Asn Phe Ser Val Ala Phe Lys  
785 790 795 800

Glu Ala Ala Arg Arg Glu Arg Gly Leu Val Asn Val Ser Ser Gln Pro  
805 810 815

Ser Leu Pro Arg Thr Leu Lys Pro Ile Gln Asp Phe Ile Phe Asn Leu  
820 825 830

Val Gly Glu  
835

<210> 5  
<211> 1947  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(1944)

<400> 5  
atg aag ttt ggt gag cac ttg agc aag tct ctt att aga cag tac agc 48  
Met Lys Phe Gly Glu His Leu Ser Lys Ser Leu Ile Arg Gln Tyr Ser  
1 5 10 15

tac tat tat att agt tat gat gat ctg aag act gag cta gaa gat aac 96  
Tyr Tyr Tyr Ile Ser Tyr Asp Asp Leu Lys Thr Glu Leu Glu Asp Asn  
20 25 30

tta tct aag aat aac ggt cag tgg acg caa gaa ttg gaa aca gat ttt 144  
Leu Ser Lys Asn Asn Gly Gln Trp Thr Gln Glu Leu Glu Thr Asp Phe  
35 40 45

tta gaa tct ttg gag atc gag tta gac aag gtt tac aca ttt tgc aaa 192  
Leu Glu Ser Leu Glu Ile Glu Leu Asp Lys Val Tyr Thr Phe Cys Lys  
50 55 60

gtt aag cat agt gaa gtt ttt aga cgt gta aaa gag gtt caa gaa caa 240  
Val Lys His Ser Glu Val Phe Arg Arg Val Lys Glu Val Gln Glu Gln  
65 70 75 80 85

## Sequence Listing PCT-JP03-00117.txt

65	70	75	80													
gtg Val	caa Gln	cat His	act Thr	ggt Val 85	cgt Arg	ttg Leu	tta Leu	gac Asp	tcc Ser 90	aat Asn	aat Asn	cct Pro	cct Pro	act Thr 95	cag Gln	288
cta Leu	gat Asp	ttt Phe	gag Glu 100	att Ile	cta Leu	gaa Glu	gaa Glu 105	gaa Glu 105	cta Leu	agt Ser	gat Asp	atc Ile	att Ile 110	gcc Ala	gat Asp	336
ggt Val	cat His	gat Asp 115	cta Leu	gca Ala	aag Lys	ttt Phe	tcg Ser 120	aga Arg	cta Leu	aac Asn	tac Tyr	act Thr 125	ggt Gly	ttc Phe	caa Gln	384
aag Lys	att Ile 130	atc Ile	aag Lys	aaa Lys	cac His	gat Asp 135	aag Lys	aag Lys	aca Thr	ggt Gly	ttt Phe 140	atc Ile	ttg Leu	aaa Lys	cca Pro	432
ggt Val 145	ttc Phe	caa Gln	ggt Val	aga Arg	tta Leu 150	gac Asp	tct Ser	aaa Lys	cca Pro	ttt Phe 155	ttc Phe	aag Lys	gaa Glu	aac Asn	tat Tyr 160	480
gac Asp	gaa Glu	cta Leu	gtc Val 165	ggt Val 165	aaa Lys	att Ile	tcc Ser	caa Gln	cta Leu 170	tat Tyr	gat Asp	att Ile	gcc Ala	aga Arg 175	act Thr	528
tca Ser	ggt Gly	cgc Arg	cca Pro 180	atc Ile	aag Lys	gga Gly	gac Asp	tca Ser 185	tct Ser	gct Ala	ggt Gly	ggg Gly 190	aag Lys 190	caa Gln	caa Gln	576
aat Asn	ttc Phe 195	ggt Val	aga Arg	cag Gln	aca Thr	aca Thr	aag Lys 200	tat Tyr	tgg Trp	ggt Val	cac His	cct Pro 205	gat Asp	aac Asn	att Ile	624
aca Thr 210	gaa Glu	ttg Leu	aag Lys	ctg Leu	atc Ile	atc Ile 215	ttg Leu	aag Lys	cat His	tta Leu	cca Pro 220	gtg Val	tta Leu	gtc Val	ttc Phe	672
aac Asn 225	act Thr	aat Asn	aag Lys	gaa Glu	ttc Phe 230	gaa Glu	aga Arg	gaa Glu	gat Asp	tcc Ser 235	gct Ala	att Ile	act Thr	tcg Ser	atc Ile 240	720
tat Tyr	ttt Phe	gat Asp	aat Asn	gaa Glu 245	aat Asn	cta Leu	gac Asp	ctt Leu	tat Tyr 250	tat Tyr	ggc Gly	aga Arg	tta Leu	aga Arg 255	aaa Lys	768
gat Asp	gaa Glu	ggt Gly	gca Ala 260	gaa Glu	gcc Ala	cac His	aga Arg	ttg Leu 265	aga Arg	tgg Trp	tat Tyr	ggg Gly	ggt Gly 270	atg Met	tct Ser	816
aca Thr	gac Asp	acg Thr 275	atc Ile	ttt Phe	gta Val	gaa Glu	aga Arg 280	aag Lys	acc Thr	cat His	aga Arg	gag Glu 285	gat Asp	tgg Trp	act Thr	864
ggt Gly 290	gag Glu	aaa Lys	tct Ser	gtc Val	aag Lys	gca Ala 295	aga Arg	ttt Phe	gcg Ala	cta Leu	aag Lys 300	gaa Glu	cgt Arg	cat His	gtt Val	912
aat Asn 305	gac Asp	ttc Phe	tta Leu	aag Lys	ggt Gly 310	aaa Lys	tat Tyr	act Thr	gtt Val	gat Asp 315	caa Gln	gta Val	ttt Phe	gcc Ala	aag Lys 320	960
atg	cgt	aaa	gaa	ggc	aag	aag	cca	atg	aac	gaa	att	gaa	aac	ttg	gag	1008

## Sequence Listing PCT-JP03-00117.txt

Met	Arg	Lys	Glu	Gly 325	Lys	Lys	Pro	Met	Asn 330	Glu	Ile	Glu	Asn	Leu 335	Glu		
gcg	tta	gca	tcc	gaa	att	caa	tac	gtc	atg	tta	aag	aaa	aag	ttg	aga	1056	
Ala	Leu	Ala	Ser 340	Glu	Ile	Gln	Tyr	Val 345	Met	Leu	Lys	Lys	Lys 350	Leu	Arg		
cct	gta	gtg	aga	tca	ttc	tac	aat	aga	act	gct	ttt	caa	tta	cct	ggt	1104	
Pro	Val	Val 355	Arg	Ser	Phe	Tyr	Asn 360	Arg	Thr	Ala	Phe	Gln 365	Leu	Pro	Gly		
gat	gca	aga	gtt	cgt	atc	tcc	ctt	gat	aca	gag	tta	act	atg	gtg	aga	1152	
Asp	Ala	Arg	Val	Arg	Ile	Ser 375	Leu	Asp	Thr	Glu	Leu 380	Thr	Met	Val	Arg		
gaa	gac	aac	ttt	gat	ggt	gtg	gat	aga	act	cat	aag	aat	tgg	agg	aga	1200	
Glu	Asp	Asn	Phe	Asp	Gly 390	Val	Asp	Arg	Thr	His 395	Lys	Asn	Trp	Arg	Arg 400		
act	gat	att	ggt	gtc	gat	tgg	cca	ttc	aag	cag	cta	gat	gac	aag	gat	1248	
Thr	Asp	Ile	Gly	Val 405	Asp	Trp	Pro	Phe	Lys 410	Gln	Leu	Asp	Asp	Lys 415	Asp		
att	tgc	cgt	ttc	cca	tat	gca	gtc	ctg	gaa	gtt	aaa	ttg	caa	act	caa	1296	
Ile	Cys	Arg	Phe 420	Pro	Tyr	Ala	Val	Leu 425	Glu	Val	Lys	Leu	Gln 430	Thr	Gln		
cta	ggt	caa	gaa	cct	cca	gag	tgg	gta	cgt	gaa	tta	gtc	ggg	tct	cac	1344	
Leu	Gly	Gln 435	Glu	Pro	Pro	Glu	Trp 440	Val	Arg	Glu	Leu	Val 445	Gly	Ser	His		
tta	gtt	gag	cca	gtc	cca	aaa	ttc	tcc	aag	ttt	att	cat	ggt	gtg	gct	1392	
Leu	Val 450	Glu	Pro	Val	Pro	Lys 455	Phe	Ser	Lys	Phe	Ile 460	His	Gly	Val	Ala		
acc	tta	cta	aat	gat	aaa	gtg	gat	tca	atc	cca	ttt	tgg	tta	cct	caa	1440	
Thr	Leu	Leu	Asn	Asp	Lys 470	Val	Asp	Ser	Ile	Pro 475	Phe	Trp	Leu	Pro	Gln 480		
atg	gat	gtt	gat	atc	agg	aaa	cct	cca	cta	cca	aca	aat	att	gaa	ata	1488	
Met	Asp	Val	Asp	Ile 485	Arg	Lys	Pro	Pro	Leu 490	Pro	Thr	Asn	Ile	Glu 495	Ile		
aca	aga	ccc	ggt	aga	tcc	gat	aac	gaa	gat	aac	gac	ttc	gat	gag	gat	1536	
Thr	Arg	Pro	Gly 500	Arg	Ser	Asp	Asn	Glu 505	Asp	Asn	Asp	Phe	Asp 510	Glu	Asp		
gat	gag	gat	gac	gct	gct	ttg	gtt	gct	gcc	atg	aca	aac	gca	ccc	ggt	1584	
Asp	Glu	Asp 515	Asp	Ala	Ala	Leu	Val 520	Ala	Ala	Met	Thr	Asn 525	Ala	Pro	Gly		
aat	tct	ctt	gat	ata	gaa	gaa	tct	gtt	ggt	tac	ggg	gct	act	tcg	gcc	1632	
Asn	Ser 530	Leu	Asp	Ile	Glu	Glu 535	Ser	Val	Gly	Tyr	Gly 540	Ala	Thr	Ser	Ala		
ccc	acc	tcc	aac	act	aat	cat	gtt	gtt	gag	agt	gct	aat	gct	gct	tat	1680	
Pro	Thr	Ser	Asn	Thr	Asn 550	His	Val	Val	Glu	Ser 555	Ala	Asn	Ala	Ala	Tyr 560		
tat	caa	aga	aag	atc	agg	aat	gcc	gaa	aat	cct	atc	tcc	aag	aaa	tac	1728	
Tyr	Gln	Arg	Lys	Ile 565	Arg	Asn	Ala	Glu	Asn 570	Pro	Ile	Ser	Lys	Lys 575	Tyr		

Sequence Listing PCT-JP03-00117.txt

tat gaa atc gtg gca ttt ttt gac cac tat ttt aac ggt gat caa ata	1776
Tyr Glu Ile Val Ala Phe Phe Asp His Tyr Phe Asn Gly Asp Gln Ile	
580 585 590	
tct aaa atc cca aaa ggt act act ttt gat act caa att cgt gcc cca	1824
Ser Lys Ile Pro Lys Gly Thr Thr Phe Asp Thr Gln Ile Arg Ala Pro	
595 600 605	
ccg gaa aga cga tat gtg tgc cag ttc gtg tgg aac caa aag ttt act	1872
Pro Glu Arg Arg Tyr Val Cys Gln Phe Val Trp Asn Gln Lys Phe Thr	
610 615 620	
ttg cca ctg aaa gaa cct acc tgt ctt ggt tgt cca tct cga tat tgt	1920
Leu Pro Leu Lys Glu Pro Thr Cys Leu Gly Cys Pro Ser Arg Tyr Cys	
625 630 635 640	
tgg gcg gtg tct cca cta ctt tat taa	1947
Trp Ala Val Ser Pro Leu Leu Tyr	
645	

<210> 6  
 <211> 648  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 6	
Met Lys Phe Gly Glu His Leu Ser Lys Ser Leu Ile Arg Gln Tyr Ser	
1 5 10 15	
Tyr Tyr Tyr Ile Ser Tyr Asp Asp Leu Lys Thr Glu Leu Glu Asp Asn	
20 25 30	
Leu Ser Lys Asn Asn Gly Gln Trp Thr Gln Glu Leu Glu Thr Asp Phe	
35 40 45	
Leu Glu Ser Leu Glu Ile Glu Leu Asp Lys Val Tyr Thr Phe Cys Lys	
50 55 60	
Val Lys His Ser Glu Val Phe Arg Arg Val Lys Glu Val Gln Glu Gln	
65 70 75 80	
Val Gln His Thr Val Arg Leu Leu Asp Ser Asn Asn Pro Pro Thr Gln	
85 90 95	
Leu Asp Phe Glu Ile Leu Glu Glu Glu Leu Ser Asp Ile Ile Ala Asp	
100 105 110	
Val His Asp Leu Ala Lys Phe Ser Arg Leu Asn Tyr Thr Gly Phe Gln	
115 120 125	
Lys Ile Ile Lys Lys His Asp Lys Lys Thr Gly Phe Ile Leu Lys Pro	
130 135 140	
Val Phe Gln Val Arg Leu Asp Ser Lys Pro Phe Phe Lys Glu Asn Tyr	
145 150 155 160	
Asp Glu Leu Val Val Lys Ile Ser Gln Leu Tyr Asp Ile Ala Arg Thr	
165 170 175	
Ser Gly Arg Pro Ile Lys Gly Asp Ser Ser Ala Gly Gly Lys Gln Gln	
180 185 190	



## Sequence Listing PCT-JP03-00117.txt

Asn Phe Val Arg Gln Thr Thr Lys Tyr Trp Val His Pro Asp Asn Ile  
 195 200 205  
 Thr Glu Leu Lys Leu Ile Ile Leu Lys His Leu Pro Val Leu Val Phe  
 210 215 220  
 Asn Thr Asn Lys Glu Phe Glu Arg Glu Asp Ser Ala Ile Thr Ser Ile  
 225 230 235 240  
 Tyr Phe Asp Asn Glu Asn Leu Asp Leu Tyr Tyr Gly Arg Leu Arg Lys  
 245 250 255  
 Asp Glu Gly Ala Glu Ala His Arg Leu Arg Trp Tyr Gly Gly Met Ser  
 260 265 270  
 Thr Asp Thr Ile Phe Val Glu Arg Lys Thr His Arg Glu Asp Trp Thr  
 275 280 285  
 Gly Glu Lys Ser Val Lys Ala Arg Phe Ala Leu Lys Glu Arg His Val  
 290 295 300  
 Asn Asp Phe Leu Lys Gly Lys Tyr Thr Val Asp Gln Val Phe Ala Lys  
 305 310 315 320  
 Met Arg Lys Glu Gly Lys Lys Pro Met Asn Glu Ile Glu Asn Leu Glu  
 325 330 335  
 Ala Leu Ala Ser Glu Ile Gln Tyr Val Met Leu Lys Lys Lys Leu Arg  
 340 345 350  
 Pro Val Val Arg Ser Phe Tyr Asn Arg Thr Ala Phe Gln Leu Pro Gly  
 355 360 365  
 Asp Ala Arg Val Arg Ile Ser Leu Asp Thr Glu Leu Thr Met Val Arg  
 370 375 380  
 Glu Asp Asn Phe Asp Gly Val Asp Arg Thr His Lys Asn Trp Arg Arg  
 385 390 395 400  
 Thr Asp Ile Gly Val Asp Trp Pro Phe Lys Gln Leu Asp Asp Lys Asp  
 405 410 415  
 Ile Cys Arg Phe Pro Tyr Ala Val Leu Glu Val Lys Leu Gln Thr Gln  
 420 425 430  
 Leu Gly Gln Glu Pro Pro Glu Trp Val Arg Glu Leu Val Gly Ser His  
 435 440 445  
 Leu Val Glu Pro Val Pro Lys Phe Ser Lys Phe Ile His Gly Val Ala  
 450 455 460  
 Thr Leu Leu Asn Asp Lys Val Asp Ser Ile Pro Phe Trp Leu Pro Gln  
 465 470 475 480  
 Met Asp Val Asp Ile Arg Lys Pro Pro Leu Pro Thr Asn Ile Glu Ile  
 485 490 495  
 Thr Arg Pro Gly Arg Ser Asp Asn Glu Asp Asn Asp Phe Asp Glu Asp  
 500 505 510  
 Asp Glu Asp Asp Ala Ala Leu Val Ala Ala Met Thr Asn Ala Pro Gly  
 515 520 525

Sequence Listing PCT-JP03-00117.txt

Asn Ser Leu Asp Ile Glu Glu Ser Val Gly Tyr Gly Ala Thr Ser Ala  
 530 535 540

Pro Thr Ser Asn Thr Asn His Val Val Glu Ser Ala Asn Ala Ala Tyr  
 545 550 555 560

Tyr Gln Arg Lys Ile Arg Asn Ala Glu Asn Pro Ile Ser Lys Lys Tyr  
 565 570 575

Tyr Glu Ile Val Ala Phe Phe Asp His Tyr Phe Asn Gly Asp Gln Ile  
 580 585 590

Ser Lys Ile Pro Lys Gly Thr Thr Phe Asp Thr Gln Ile Arg Ala Pro  
 595 600 605

Pro Glu Arg Arg Tyr Val Cys Gln Phe Val Trp Asn Gln Lys Phe Thr  
 610 615 620

Leu Pro Leu Lys Glu Pro Thr Cys Leu Gly Cys Pro Ser Arg Tyr Cys  
 625 630 635 640

Trp Ala Val Ser Pro Leu Leu Tyr  
 645

<210> 7  
 <211> 390  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> CDS  
 <222> (1)..(387)

<400> 7  
 atg tct tca gca cca tta tta caa aga aca cct ggg aaa aag atc gct 48  
 Met Ser Ser Ala Pro Leu Leu Gln Arg Thr Pro Gly Lys Lys Ile Ala  
 1 5 10 15

ttg ccc aca cga gtt gag cca aaa gtg ttc ttt gcc aat gag cgt acc 96  
 Leu Pro Thr Arg Val Glu Pro Lys Val Phe Phe Ala Asn Glu Arg Thr  
 20 25 30

ttt ttg tcg tgg ttg aac ttt aca gtt atg ctg gga ggc ctt ggt gta 144  
 Phe Leu Ser Trp Leu Asn Phe Thr Val Met Leu Gly Gly Leu Gly Val  
 35 40 45

ggt tta ctg aat ttt ggt gac aag ata ggt agg gtc agt gca gga cta 192  
 Gly Leu Leu Asn Phe Gly Asp Lys Ile Gly Arg Val Ser Ala Gly Leu  
 50 55 60

ttt act ttt gtt gcc atg ggt aca atg ata tac gcg ctt gta aca tac 240  
 Phe Thr Phe Val Ala Met Gly Thr Met Ile Tyr Ala Leu Val Thr Tyr  
 65 70 75 80

cac tgg aga gct gct gcg att aga cgt aga gga tca ggt cct tat gat 288  
 His Trp Arg Ala Ala Ala Ile Arg Arg Arg Gly Ser Gly Pro Tyr Asp  
 85 90 95

gac aga ttg ggg ccc act ttg ttg tgc ttt ttc tta ttg gtt gct gtc 336  
 Asp Arg Leu Gly Pro Thr Leu Leu Cys Phe Phe Leu Leu Val Ala Val  
 100 105 110

Sequence Listing PCT-JP03-00117.txt

att atc aac ttt ata tta aga ttg aag tac aat gac gct aac act aag 384  
 ile ile asn phe ile leu arg leu lys tyr asn asp ala asn thr lys  
           115                          120                          125

tta tga 390  
 leu

<210> 8  
 <211> 129  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 8  
 Met Ser Ser Ala Pro Leu Leu Gln Arg Thr Pro Gly Lys Lys Ile Ala  
   1                  5                          10                          15  
 Leu Pro Thr Arg Val Glu Pro Lys Val Phe Phe Ala Asn Glu Arg Thr  
                   20                          25                          30  
 Phe Leu Ser Trp Leu Asn Phe Thr Val Met Leu Gly Gly Leu Gly Val  
                   35                          40                          45  
 Gly Leu Leu Asn Phe Gly Asp Lys Ile Gly Arg Val Ser Ala Gly Leu  
   50                          55                          60  
 Phe Thr Phe Val Ala Met Gly Thr Met Ile Tyr Ala Leu Val Thr Tyr  
   65                  70                          75                          80  
 His Trp Arg Ala Ala Ile Arg Arg Arg Gly Ser Gly Pro Tyr Asp  
                   85                          90                          95  
 Asp Arg Leu Gly Pro Thr Leu Leu Cys Phe Phe Leu Leu Val Ala Val  
                   100                          105                          110  
 Ile Ile Asn Phe Ile Leu Arg Leu Lys Tyr Asn Asp Ala Asn Thr Lys  
           115                          120                          125  
 Leu

<210> 9  
 <211> 2025  
 <212> DNA  
 <213> Saccharomyces cerevisiae

<220>  
 <221> CDS  
 <222> (1)..(2022)

<400> 9  
 atg gtt gta gtg ggt aag agt gaa gtg cgc aat gta agc atg agt agg 48  
 Met Val Val Val Gly Lys Ser Glu Val Arg Asn Val Ser Met Ser Arg  
   1                  5                          10                          15  
 ccg aag aag aaa tca ttg att gcc atc ctg tcg acc tgt gtt ttg ttt 96  
 Pro Lys Lys Lys Ser Leu Ile Ala Ile Leu Ser Thr Cys Val Leu Phe  
                   20                          25                          30  
 ttc ctc gtg ttt ata att ggt gct aaa ttt caa tat gtt tcc gtt ttc 144  
   Page 19

## Sequence Listing PCT-JP03-00117.txt

Phe	Leu	Val	Phe	Ile	Ile	Gly	Ala	Lys	Phe	Gln	Tyr	Val	Ser	Val	Phe		
		35					40					45					
tcc	aaa	ttc	tta	gat	gac	agg	ggg	gac	aac	gag	tca	ctt	caa	ttg	ctc	192	
Ser	Lys	Phe	Leu	Asp	Asp	Arg	Gly	Asp	Asn	Glu	Ser	Leu	Gln	Leu	Leu		
	50					55				60							
aat	gac	ata	gaa	ttt	aca	agg	cta	gga	ctg	aca	cct	agg	gag	cca	gta	240	
Asn	Asp	Ile	Glu	Phe	Thr	Arg	Leu	Gly	Leu	Thr	Pro	Arg	Glu	Pro	Val		
65					70					75					80		
att	atc	aaa	gac	gta	aag	aca	ggg	aag	gag	aga	aaa	tta	cat	gga	cgg	288	
Ile	Ile	Lys	Asp	Val	Lys	Thr	Gly	Lys	Glu	Arg	Lys	Leu	His	Gly	Arg		
				85					90					95			
ttc	ctt	cat	att	acc	gat	att	cat	cct	gac	cct	tat	tat	gtg	gaa	gga	336	
Phe	Leu	His	Ile	Thr	Asp	Ile	His	Pro	Asp	Pro	Tyr	Tyr	Val	Glu	Gly		
			100					105					110				
agc	tct	att	gat	gca	gtt	tgt	cac	aca	gga	aaa	cca	agc	aaa	aaa	aag	384	
Ser	Ser	Ile	Asp	Ala	Val	Cys	His	Thr	Gly	Lys	Pro	Ser	Lys	Lys	Lys		
		115				120						125					
gat	gtg	gca	ccc	aag	ttt	ggg	aag	gca	atg	tct	gga	tgt	gat	tct	ccc	432	
Asp	Val	Ala	Pro	Lys	Phe	Gly	Lys	Ala	Met	Ser	Gly	Cys	Asp	Ser	Pro		
	130					135					140						
gtt	att	tta	atg	gaa	gaa	act	ctg	aga	tgg	att	aaa	gaa	aat	ctt	aga	480	
Val	Ile	Leu	Met	Glu	Glu	Thr	Leu	Arg	Trp	Ile	Lys	Glu	Asn	Leu	Arg		
				150						155					160		
gat	aag	att	gat	ttt	gtc	att	tgg	acg	ggt	gat	aat	atc	aga	cat	gac	528	
Asp	Lys	Ile	Asp	Phe	Val	Ile	Trp	Thr	Gly	Asp	Asn	Ile	Arg	His	Asp		
				165					170					175			
aat	gac	cgg	aaa	cat	cca	aga	aca	gaa	gca	caa	att	ttt	gat	atg	aac	576	
Asn	Asp	Arg	Lys	His	Pro	Arg	Thr	Glu	Ala	Gln	Ile	Phe	Asp	Met	Asn		
			180					185					190				
aat	atc	gtt	gct	gat	aaa	atg	aca	gaa	tta	ttt	agt	gct	ggc	aat	gaa	624	
Asn	Ile	Val	Ala	Asp	Lys	Met	Thr	Glu	Leu	Phe	Ser	Ala	Gly	Asn	Glu		
		195				200						205					
gaa	gat	cca	aga	gat	ttt	gat	gtg	tct	gtc	att	cca	agt	ctt	gga	aac	672	
Glu	Asp	Pro	Arg	Asp	Phe	Asp	Val	Ser	Val	Ile	Pro	Ser	Leu	Gly	Asn		
	210					215					220						
aat	gat	gtc	ttt	cca	cat	aac	atg	ttt	gca	cta	gga	cca	act	cta	caa	720	
Asn	Asp	Val	Phe	Pro	His	Asn	Met	Phe	Ala	Leu	Gly	Pro	Thr	Leu	Gln		
				225		230				235					240		
act	aga	gaa	tat	tat	agg	att	tgg	aaa	aat	ttt	gtt	ccg	cag	cag	cag	768	
Thr	Arg	Glu	Tyr	Tyr	Arg	Ile	Trp	Lys	Asn	Phe	Val	Pro	Gln	Gln	Gln		
				245					250					255			
caa	aga	act	ttt	gat	agg	agt	gct	tca	ttt	ttg	act	gaa	gtt	att	cca	816	
Gln	Arg	Thr	Phe	Asp	Arg	Ser	Ala	Ser	Phe	Leu	Thr	Glu	Val	Ile	Pro		
			260					265					270				
ggg	aag	ctt	gct	gtc	ctg	tca	att	aac	acg	ctg	tac	tta	ttc	aag	gcc	864	
Gly	Lys	Leu	Ala	Val	Leu	Ser	Ile	Asn	Thr	Leu	Tyr	Leu	Phe	Lys	Ala		
		275					280					285					

## Sequence Listing PCT-JP03-00117.txt

aat	ccg	tta	gtt	gac	aat	tgt	aat	tca	aaa	aaa	gaa	cca	ggt	tac	caa	912
Asn	Pro	Leu	Val	Asp	Asn	Cys	Asn	Ser	Lys	Lys	Glu	Pro	Gly	Tyr	Gln	
	290					295					300					
ctt	tta	ctt	tgg	ttc	ggt	tat	gta	tta	gaa	gaa	cta	agg	agt	agg	gga	960
Leu	Leu	Leu	Trp	Phe	Gly	Tyr	Val	Leu	Glu	Glu	Leu	Arg	Ser	Arg	Gly	
	305				310					315					320	
atg	aaa	gta	tgg	tta	agt	gga	cat	gta	cct	cca	atc	gca	aaa	aat	ttc	1008
Met	Lys	Val	Trp	Leu	Ser	Gly	His	Val	Pro	Pro	Ile	Ala	Lys	Asn	Phe	
				325					330					335		
gat	cag	tcg	tgc	tac	gat	aag	ttc	acg	cta	tgg	act	cac	gaa	tac	agg	1056
Asp	Gln	Ser	Cys	Tyr	Asp	Lys	Phe	Thr	Leu	Trp	Thr	His	Glu	Tyr	Arg	
			340					345					350			
gat	ata	atc	att	gga	gga	tta	tac	ggt	cac	atg	aat	att	gac	cac	ttc	1104
Asp	Ile	Ile	Ile	Gly	Gly	Leu	Tyr	Gly	His	Met	Asn	Ile	Asp	His	Phe	
		355					360					365				
atc	cca	acg	gat	ggt	aaa	aaa	gct	aga	aaa	tcg	tta	ttg	aaa	gcc	atg	1152
Ile	Pro	Thr	Asp	Gly	Lys	Lys	Ala	Arg	Lys	Ser	Leu	Leu	Lys	Ala	Met	
	370					375					380					
gag	caa	tcc	act	cgt	gtt	caa	caa	gga	gaa	gac	agt	aat	gaa	gag	gac	1200
Glu	Gln	Ser	Thr	Arg	Val	Gln	Gln	Gly	Glu	Asp	Ser	Asn	Glu	Glu	Asp	
	385				390					395					400	
gaa	gaa	act	gaa	ttg	aat	aga	att	ctg	gat	cac	gct	atg	gcg	gca	aaa	1248
Glu	Glu	Thr	Glu	Leu	Asn	Arg	Ile	Leu	Asp	His	Ala	Met	Ala	Ala	Lys	
				405					410					415		
gaa	gtt	ttt	tta	atg	gga	gcg	aaa	cca	tct	aac	aaa	gaa	gca	tat	atg	1296
Glu	Val	Phe	Leu	Met	Gly	Ala	Lys	Pro	Ser	Asn	Lys	Glu	Ala	Tyr	Met	
			420					425					430			
aac	acc	gtc	cgc	gac	aca	tac	tat	cgg	aaa	gtg	tgg	aat	aag	ctg	gaa	1344
Asn	Thr	Val	Arg	Asp	Thr	Tyr	Tyr	Arg	Lys	Val	Trp	Asn	Lys	Leu	Glu	
		435					440					445				
aga	gtg	gat	gaa	aaa	aat	gtt	gaa	aat	gag	aag	aaa	aag	aaa	gaa	aag	1392
Arg	Val	Asp	Glu	Lys	Asn	Val	Glu	Asn	Glu	Lys	Lys	Lys	Lys	Glu	Lys	
	450					455					460					
aag	gac	aaa	aaa	aag	aaa	aag	cca	atc	act	aga	aaa	gag	ctc	att	gaa	1440
Lys	Asp	Lys	Lys	Lys	Lys	Lys	Pro	Ile	Thr	Arg	Lys	Glu	Leu	Ile	Glu	
	465				470					475					480	
cgc	tat	tcc	att	gtg	aac	ata	ggt	ggt	tca	gtc	att	cca	act	ttc	aat	1488
Arg	Tyr	Ser	Ile	Val	Asn	Ile	Gly	Gly	Ser	Val	Ile	Pro	Thr	Phe	Asn	
				485					490					495		
cct	tcc	ttt	agg	atc	tgg	gaa	tat	aac	atc	acc	gac	ata	gtg	aat	gac	1536
Pro	Ser	Phe	Arg	Ile	Trp	Glu	Tyr	Asn	Ile	Thr	Asp	Ile	Val	Asn	Asp	
			500					505					510			
tcc	aat	ttt	gca	gtt	tcg	gag	tat	aag	ccc	tgg	gat	gaa	ttt	ttc	gag	1584
Ser	Asn	Phe	Ala	Val	Ser	Glu	Tyr	Lys	Pro	Trp	Asp	Glu	Phe	Phe	Glu	
		515					520					525				
tca	cta	aat	aag	att	atg	gaa	gac	tct	ttg	cta	gaa	gat	gaa	atg	gac	1632
Ser	Leu	Asn	Lys	Ile	Met	Glu	Asp	Ser	Leu	Leu	Glu	Asp	Glu	Met	Asp	
	530					535						540				

Sequence Listing PCT-JP03-00117.txt

agc agt aat atc gag gtt ggg atc aac cgc gag aag atg ggc gaa aag	1680
Ser Ser Asn Ile Glu Val Gly Ile Asn Arg Glu Lys Met Gly Glu Lys	
545 550 555 560	
aaa aac aag aag aaa aag aaa aat gac aag act atg cca att gag atg	1728
Lys Asn Lys Lys Lys Lys Lys Asn Asp Lys Thr Met Pro Ile Glu Met	
565 570 575	
cca gac aaa tac gaa ctc ggc cct gca tat gta ccg cag tta ttc act	1776
Pro Asp Lys Tyr Glu Leu Gly Pro Ala Tyr Val Pro Gln Leu Phe Thr	
580 585 590	
ccg acg cgt ttc gtc caa ttc tac gcc gac ttg gaa aaa atc aat caa	1824
Pro Thr Arg Phe Val Gln Phe Tyr Ala Asp Leu Glu Lys Ile Asn Gln	
595 600 605	
gaa tta cat aat tca ttt gtt gaa tct aag gat att ttc agg tat gag	1872
Glu Leu His Asn Ser Phe Val Glu Ser Lys Asp Ile Phe Arg Tyr Glu	
610 615 620	
ata gaa tat acc tca gac gag aaa cca tac tca atg gat tcg tta aca	1920
Ile Glu Tyr Thr Ser Asp Glu Lys Pro Tyr Ser Met Asp Ser Leu Thr	
625 630 635 640	
gta gga agt tat ttg gat ctt gca ggc aga tta tac gaa aac aaa cct	1968
Val Gly Ser Tyr Leu Asp Leu Ala Gly Arg Leu Tyr Glu Asn Lys Pro	
645 650 655	
gca tgg gaa aaa tac gtc gaa tgg tca ttt gcg tct tct gga tat aaa	2016
Ala Trp Glu Lys Tyr Val Glu Trp Ser Phe Ala Ser Ser Gly Tyr Lys	
660 665 670	
gat gat taa	2025
Asp Asp	

<210> 10  
 <211> 674  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 10  
 Met Val Val Val Gly Lys Ser Glu Val Arg Asn Val Ser Met Ser Arg  
 1 5 10 15  
 Pro Lys Lys Lys Ser Leu Ile Ala Ile Leu Ser Thr Cys Val Leu Phe  
 20 25 30  
 Phe Leu Val Phe Ile Ile Gly Ala Lys Phe Gln Tyr Val Ser Val Phe  
 35 40 45  
 Ser Lys Phe Leu Asp Asp Arg Gly Asp Asn Glu Ser Leu Gln Leu Leu  
 50 55 60  
 Asn Asp Ile Glu Phe Thr Arg Leu Gly Leu Thr Pro Arg Glu Pro Val  
 65 70 75 80  
 Ile Ile Lys Asp Val Lys Thr Gly Lys Glu Arg Lys Leu His Gly Arg  
 85 90 95  
 Phe Leu His Ile Thr Asp Ile His Pro Asp Pro Tyr Tyr Val Glu Gly  
 100 105 110

Sequence Listing PCT-JP03-00117.txt

Ser Ser Ile Asp Ala Val Cys His Thr Gly Lys Pro Ser Lys Lys Lys  
115 120 125

Asp Val Ala Pro Lys Phe Gly Lys Ala Met Ser Gly Cys Asp Ser Pro  
130 135 140

Val Ile Leu Met Glu Glu Thr Leu Arg Trp Ile Lys Glu Asn Leu Arg  
145 150 155 160

Asp Lys Ile Asp Phe Val Ile Trp Thr Gly Asp Asn Ile Arg His Asp  
165 170 175

Asn Asp Arg Lys His Pro Arg Thr Glu Ala Gln Ile Phe Asp Met Asn  
180 185 190

Asn Ile Val Ala Asp Lys Met Thr Glu Leu Phe Ser Ala Gly Asn Glu  
195 200 205

Glu Asp Pro Arg Asp Phe Asp Val Ser Val Ile Pro Ser Leu Gly Asn  
210 215 220

Asn Asp Val Phe Pro His Asn Met Phe Ala Leu Gly Pro Thr Leu Gln  
225 230 235 240

Thr Arg Glu Tyr Tyr Arg Ile Trp Lys Asn Phe Val Pro Gln Gln Gln  
245 250 255

Gln Arg Thr Phe Asp Arg Ser Ala Ser Phe Leu Thr Glu Val Ile Pro  
260 265 270

Gly Lys Leu Ala Val Leu Ser Ile Asn Thr Leu Tyr Leu Phe Lys Ala  
275 280 285

Asn Pro Leu Val Asp Asn Cys Asn Ser Lys Lys Glu Pro Gly Tyr Gln  
290 295 300

Leu Leu Leu Trp Phe Gly Tyr Val Leu Glu Glu Leu Arg Ser Arg Gly  
305 310 315 320

Met Lys Val Trp Leu Ser Gly His Val Pro Pro Ile Ala Lys Asn Phe  
325 330 335

Asp Gln Ser Cys Tyr Asp Lys Phe Thr Leu Trp Thr His Glu Tyr Arg  
340 345 350

Asp Ile Ile Ile Gly Gly Leu Tyr Gly His Met Asn Ile Asp His Phe  
355 360 365

Ile Pro Thr Asp Gly Lys Lys Ala Arg Lys Ser Leu Leu Lys Ala Met  
370 375 380

Glu Gln Ser Thr Arg Val Gln Gln Gly Glu Asp Ser Asn Glu Glu Asp  
385 390 395 400

Glu Glu Thr Glu Leu Asn Arg Ile Leu Asp His Ala Met Ala Ala Lys  
405 410 415

Glu Val Phe Leu Met Gly Ala Lys Pro Ser Asn Lys Glu Ala Tyr Met  
420 425 430

Asn Thr Val Arg Asp Thr Tyr Tyr Arg Lys Val Trp Asn Lys Leu Glu  
435 440 445

Sequence Listing PCT-JP03-00117.txt

Arg Val Asp Glu Lys Asn Val Glu Asn Glu Lys Lys Lys Lys Glu Lys  
 450 455 460

Lys Asp Lys Lys Lys Lys Lys Pro Ile Thr Arg Lys Glu Leu Ile Glu  
 465 470 475 480

Arg Tyr Ser Ile Val Asn Ile Gly Gly Ser Val Ile Pro Thr Phe Asn  
 485 490 495

Pro Ser Phe Arg Ile Trp Glu Tyr Asn Ile Thr Asp Ile Val Asn Asp  
 500 505 510

Ser Asn Phe Ala Val Ser Glu Tyr Lys Pro Trp Asp Glu Phe Phe Glu  
 515 520 525

Ser Leu Asn Lys Ile Met Glu Asp Ser Leu Leu Glu Asp Glu Met Asp  
 530 535 540

Ser Ser Asn Ile Glu Val Gly Ile Asn Arg Glu Lys Met Gly Glu Lys  
 545 550 555 560

Lys Asn Lys Lys Lys Lys Lys Asn Asp Lys Thr Met Pro Ile Glu Met  
 565 570 575

Pro Asp Lys Tyr Glu Leu Gly Pro Ala Tyr Val Pro Gln Leu Phe Thr  
 580 585 590

Pro Thr Arg Phe Val Gln Phe Tyr Ala Asp Leu Glu Lys Ile Asn Gln  
 595 600 605

Glu Leu His Asn Ser Phe Val Glu Ser Lys Asp Ile Phe Arg Tyr Glu  
 610 615 620

Ile Glu Tyr Thr Ser Asp Glu Lys Pro Tyr Ser Met Asp Ser Leu Thr  
 625 630 635 640

Val Gly Ser Tyr Leu Asp Leu Ala Gly Arg Leu Tyr Glu Asn Lys Pro  
 645 650 655

Ala Trp Glu Lys Tyr Val Glu Trp Ser Phe Ala Ser Ser Gly Tyr Lys  
 660 665 670

Asp Asp

<210> 11  
 <211> 405  
 <212> DNA  
 <213> Rattus rattus

<220>  
 <221> CDS  
 <222> (1)..(402)

<400> 11  
 atg gcc gag cag tca gac aag gat gtg aag tac tac act ctg gag gag 48  
 Met Ala Glu Gln Ser Asp Lys Asp Val Lys Tyr Tyr Thr Leu Glu Glu  
 1 5 10 15

att cag aag cac aaa gac agc aag agc acc tgg gtg atc cta cat cat 96  
 Page 24



## Sequence Listing PCT-JP03-00117.txt

Ile Gln Lys His Lys Asp Ser Lys Ser Thr Trp Val Ile Leu His His  
 20 25 30  
 aag gtg tac gat ctg acc aag ttt ctc gaa gag cat cct ggt ggg gaa 144  
 Lys Val Tyr Asp Leu Thr Lys Phe Leu Glu Glu His Pro Gly Gly Glu  
 35 40 45  
 gaa gtc cta aga gag caa gct ggg ggt gat gct act gag aac ttt gag 192  
 Glu Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu  
 50 55 60  
 gac gtc ggg cac tct acg gat gca cga gaa ctg tcc aaa aca tac atc 240  
 Asp Val Gly His Ser Thr Asp Ala Arg Glu Leu Ser Lys Thr Tyr Ile  
 65 70 75 80  
 atc ggg gag ctg cat cca gat gac aga tca aag ata gcc aag cct tcg 288  
 Ile Gly Glu Leu His Pro Asp Asp Arg Ser Lys Ile Ala Lys Pro Ser  
 85 90 95  
 gaa acc ctt atc act act gtc gag tct aat tcc agt tgg tgg acc aac 336  
 Glu Thr Leu Ile Thr Thr Val Glu Ser Asn Ser Ser Trp Trp Thr Asn  
 100 105 110  
 tgg gtg atc cca gcc atc tca gcc ctg gtg gta gct ctg atg tat cgc 384  
 Trp Val Ile Pro Ala Ile Ser Ala Leu Val Val Ala Leu Met Tyr Arg  
 115 120 125  
 ctc tac atg gca gaa gat taa 405  
 Leu Tyr Met Ala Glu Asp  
 130

<210> 12  
 <211> 134  
 <212> PRT  
 <213> Rattus rattus

<400> 12  
 Met Ala Glu Gln Ser Asp Lys Asp Val Lys Tyr Tyr Thr Leu Glu Glu  
 1 5 10 15  
 Ile Gln Lys His Lys Asp Ser Lys Ser Thr Trp Val Ile Leu His His  
 20 25 30  
 Lys Val Tyr Asp Leu Thr Lys Phe Leu Glu Glu His Pro Gly Gly Glu  
 35 40 45  
 Glu Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu  
 50 55 60  
 Asp Val Gly His Ser Thr Asp Ala Arg Glu Leu Ser Lys Thr Tyr Ile  
 65 70 75 80  
 Ile Gly Glu Leu His Pro Asp Asp Arg Ser Lys Ile Ala Lys Pro Ser  
 85 90 95  
 Glu Thr Leu Ile Thr Thr Val Glu Ser Asn Ser Ser Trp Trp Thr Asn  
 100 105 110  
 Trp Val Ile Pro Ala Ile Ser Ala Leu Val Val Ala Leu Met Tyr Arg  
 115 120 125  
 Leu Tyr Met Ala Glu Asp

## Sequence Listing PCT-JP03-00117.txt

130

<210> 13  
 <211> 363  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> CDS  
 <222> (1)..(360)

<400> 13  
 atg cct aaa gtt tac agt tac caa gaa gtt gcc gaa cac aat ggc cca 48  
 Met Pro Lys Val Tyr Ser Tyr Gln Glu Val Ala Glu His Asn Gly Pro  
 1 5 10 15  
 gaa aat ttc tgg att atc atc gat gac aaa gtt tac gat gtt tct caa 96  
 Glu Asn Phe Trp Ile Ile Ile Asp Asp Lys Val Tyr Asp Val Ser Gln  
 20 25 30  
 ttc aaa gat gaa cat cca ggt ggt gat gaa att ata atg gat ttg ggt 144  
 Phe Lys Asp Glu His Pro Gly Gly Asp Glu Ile Ile Met Asp Leu Gly  
 35 40 45  
 gga caa gat gct aca gaa agc ttt gtc gat atc ggt cat tct gac gaa 192  
 Gly Gln Asp Ala Thr Glu Ser Phe Val Asp Ile Gly His Ser Asp Glu  
 50 55 60  
 gca ttg aga cta ctg aaa ggt tta tac att ggt gac gtt gac aag acc 240  
 Ala Leu Arg Leu Leu Lys Gly Leu Tyr Ile Gly Asp Val Asp Lys Thr  
 65 70 75  
 agt gag cgc gtt tct gtg gaa aag gta tct acc tct gaa aac caa agt 288  
 Ser Glu Arg Val Ser Val Glu Lys Val Ser Thr Ser Glu Asn Gln Ser  
 85 90 95  
 aaa ggt agt ggt aca ttg gtt gtc ata ttg gcc att tta atg cta ggt 336  
 Lys Gly Ser Gly Thr Leu Val Val Ile Leu Ala Ile Leu Met Leu Gly  
 100 105 110  
 gtt gct tat tat ttg ttg aac gaa taa 363  
 Val Ala Tyr Tyr Leu Leu Asn Glu  
 115 120

<210> 14  
 <211> 120  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 14  
 Met Pro Lys Val Tyr Ser Tyr Gln Glu Val Ala Glu His Asn Gly Pro  
 1 5 10 15  
 Glu Asn Phe Trp Ile Ile Ile Asp Asp Lys Val Tyr Asp Val Ser Gln  
 20 25 30  
 Phe Lys Asp Glu His Pro Gly Gly Asp Glu Ile Ile Met Asp Leu Gly  
 35 40 45  
 Gly Gln Asp Ala Thr Glu Ser Phe Val Asp Ile Gly His Ser Asp Glu

Sequence Listing PCT-JP03-00117.txt

50

55

60

Ala Leu Arg Leu Leu Lys Gly Leu Tyr Ile Gly Asp Val Asp Lys Thr  
65 70 75 80  
Ser Glu Arg Val Ser Val Glu Lys Val Ser Thr Ser Glu Asn Gln Ser  
85 90 95  
Lys Gly Ser Gly Thr Leu Val Val Ile Leu Ala Ile Leu Met Leu Gly  
100 105 110  
Val Ala Tyr Tyr Leu Leu Asn Glu  
115 120